

**PM1-AHAS1 nucleotide sequence(SEQ ID NO: 1) and
translated amino acid sequence (SEQ ID NO: 101)**

1 TCATCATCTCTCTCTCTCAAAACCATGGCGGCGGCAACATCGTCTTCTCCGATCTCCTTAACCGCTAAACCTTCTTCCAAATCCCCTCTACCCATTTC
M A A A T S S S P I S L T A K P S S K S P L P I S

101 GATTCTCCCTTCCCTTCTCCTTAACCCACAGAAAGACTCTCCCGTCTCCACCGTCTCTCGCCATCTCCGCCGTTCTCAAACCTCACCCGTCAATGTGCGC
R F S L P F S L T P Q K D S S R L H R P L A I S A V L N S P V N V A

201 ACCTCCTTCCCCTGAAAAAACCGACAAGAACAAGACTTTTCGTCTCCCGCTACGCTCCCGACGAGCCCCGAAGGGTGCTGATATCCTCGTCGAAGCCCTC
P P S P E K T D K N K T F V S R Y A P D E P R K G A D I L V E A L

301 GAGCGTCAAGGCGTCGAAACCGTCTTTGCTTATCCCGGAGGTGCTTCCATGGAGATCCACCAAGCCTTGACTCGCTCCTCCACCATCCGTAACGTCCTTC
E R Q G V E T V F A Y P G G A S M E I H Q A L T R S S T I R N V L

401 CCCGTCACGAACAAGGAGGAGTCTTCGCGCGGAGGGTTACGCTCGTTCTCCGGCAAACCGGAATCTGCATAGCCACTTCGGGTCGCGGAGCTACCAA
P R H E Q G G V F A A E G Y A R S S G K P G I C I A T S G P G A T N

501 CCTCGTCAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTCTTGTCGCCATTACAGGACAGGTCCCTCGCGGGATGATCGGTACTGACGCCTTCCAA
L V S G L A D A M L D S V P L V A I T G Q V P R R M I G T D A F Q

601 GAGACACCAATCGTTGAGTAACGAGGTCTATTACGAAACATAACTATCTGGTGATGGATGTTGATGACATACCTAGGATCGTTCAAGAAGCATTCTTTC
E T P I V E V T R S I T K H N Y L V M D V D D I P R I V Q E A F F

701 TAGCTACTTCCGGTAGACCCGGACCGGTTTTGGTTGATGTTCTTAAGGATATTAGCAGCAGCTTGCATTCTTAAGTGGGATCAACCTATGCGCTTGCC
L A T S G R P G P V L V D V P K D I Q Q Q L A I P N W D Q P M R L P

801 TGGCTACATGTCTAGGTTGCCTCAGCCWCCGGAAGTTTCTCAGTTAGGTACAGATCGTTAGGTTGATCTCGGAGTCTAAGAGGCCTGTTTTGTACGTTGGT
G Y M S R L P Q X P E V S Q L G Q I V R L I S E S K R P V L Y V G

901 GGTGGAAGCTTGAACCTCAGTGAAGAAGTGGGGAGATTGTGCGAGCTTACTGGGATCCCTGTTGCGAGTACGTTGATGGGGCTTGGCTCTTATCCTTGTA
G G S L N S S E E L G R F V E L T G I P V A S T L M G L G S Y P C

1001 ACGATGAGTTGTCCCTGCAGATGCTTGGCATGCACGGGACTGTGTATGCTAACTACGCTGTGGAGCATAGTGATTGTTGCTGGCGTTTGGTGTAGGTT
N D E L S L Q M L G M H G T V Y A N Y A V E H S D L L L A F G V R F

1101 TGATGACCGTGTACGGGAAAGCTCGAGGCTTTCTCGTAGCAGGGCTAAAATTGTGCACATAGACATTGATTCTGCTGAGATTGGGAAGAATAAGACACCT
D D R V T G K L E A F A S R A K I V H I D I D S A E I G K N K T P

1201 CACGTGTCTGTGTGTGGTGATGTAAAGCTGGCTTTGCAAGGGATGAACAAGGTTCTTGAGAACCGGGGAGGAGCTCAAGCTTGATTTCCGTTGTTTGGGA
H V S V C G D V K L A L Q G M N K V L E N R A E E L K L D F G V W

1301 GGAGTGAGTTGAGCGAGCAGAAACAGAAGTTCCCTTTGAGCTTCAAAACGTTTGGAGAAGCCATTCTCCGAGTACGCGATTGAGATCCTCGACGAGCT
R S E L S E Q K Q K F P L S F K T F G E A I P P Q Y A I Q I L D E L

1401 AACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCGTCAGATGTGGGCGGCGCAGTTTACAAAGTACAGGAAGCCGAGACAGTGGCTGTCTGCA
T E G K A I I S T G V G Q R Q M W A A Q F Y K Y R K P R Q W L S S

1501 TCAGGCCTCGGAGCTATGGGTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCTGATGCGATTGTTGTGGATATTGACGGTGATGGAAGCT
S G L G A M G F G L P A A I G A S V A N P D A I V V D I D G D G S

1601 TCATAATGAACGTTCAAGAGCTGGCCACAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTGTAAACAACAGCATCTTGGGATGGTCATGCAATG
F I M N V Q E L A T I R V E N L P V K I L L L N N Q H L G M V M Q W

1701 GGAAGATCGGTTCTACAAAGCTAACAGAGCTCACACTTATCTCGGGGACCCGGCAAGGGAGAACGAGATCTTCCCTAACATGCTGCAGTTTGCAGGAGCT
E D R F Y K A N R A H T Y L G D P A R E N E I F P N M L Q F A G A

1801 TGCGGGATTCCAGCTGCGAGAGTGACGAAGAAAGAAGAACTCCGAGAAGCTATTACAGACAATGCTGGATACACCAGGACCATACTGTTGGATGTGATAT
C G I P A A R V T K K E E L R E A I Q T M L D T P G P Y L L D V I

1901 GTCCGCACCAAGAACATGTGTTACCGATGATCCCAATGGTGGCACTTTCAAAGATGTAATAACAGAAGGGGATGGTCGCACTAAGTACTGAGAGATTMA
C P H Q E H V L P M I P N G G T F K D V I T E G D G R T K Y

2001 GCTGGTGATCGATCATATGGTAAAAGACTTAGTTTCAGTTTCCAGTTTCTTTTGTGTGGTAATTTGGGTTTGTGAGTTGTTGT

Figure 1A

**PM2-AHAS3 nucleotide sequence (SEQ ID NO:2) and
translated amino acid sequence (SEQ ID NO: 102)**

1 TTCATCATMTCTCTCTCATTTCTCTCTCTCTCATCTAACCATGGCGGCGGCAACATCGTCTTCTCCGATCTCCTTAACCGCTAAACCTTCTTCCAAAT
M A A A T S S S P I S L T A K P S S K

101 CCCCTCTACCCATTTCCAGATTCTCCCTTCCCTTCTCCTTAACCCACAGAAACCTCCTCCCGTCTCCACCGTCCACTCGCCATCTCCGCCGTTCTCAA
S P L P I S R F S L P F S L T P Q K P S S R L H R P L A I S A V L N

201 CTCACCCGTCAATGTCGCACCTGAAAAAACCGACAAGATCAAGACTTTTCATCTCCCGCTACGCTCCCGACGAGCCCCGCAAGGGTGCTGATATCCTCGTG
S P V N V A P E K T D K I K T F I S R Y A P D E P R K G A D I L V

301 GAAGCCCTCGAGCGTCAAGGCGTCGAAACCGTCTTCGCTTATCCCGAGGTGCCTCCATGGAGATCCACCAAGCCTTGACTCGTCTCTCCACCATCCGTA
E A L E R Q G V E T V F A Y P G G A S M E I H Q A L T R S S T I R

401 ACGTCTCCCCCGTCAAGAACAGGAGGAGTCTTCGCCCGGAGGGTTACGCTCGTTCCTCCGGCAAACCGGAATCTGCATAGCCACTTCGGGTCCCGG
N V L P R H E Q G G V F A A E G Y A R S S G K P G I C I A T S G P G

501 AGCTACCAACCTCGTCAGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCCATCACAGGACAGGTCCCTCGCCGGATGATCGGTACTGAC
A T N L V S G L A D A M L D S V P L V A I T G Q V P R R M I G T D

601 GCGTTCCAAGAGACGCCAATCGTTGAGGTAACGAGGTCTATTACGAAACATAACTATCTGGTGATGGATGTTGATGACATACCTAGGATCGTTCAAGAAG
A F Q E T P I V E V T R S I T K H N Y L V M D V D D I P R I V Q E

701 CATTCTTTCTAGTACTTCCGGTAGACCCGGACCGGTTTGGTTGATGTTCTCTAAGGATATTGAGCAGCAGCTTGCGATTCTAAGTGGGATCAACCTAT
A F F L A T S G R P G P V L V D V P K D I Q Q Q L A I P N W D Q P M

801 GCGCTTGCCTGGCTACATGTCTAGGCTGCCTCAGCCACCGGAAGTTTCTCAGTTAGGCCAGATCGTTAGGTTGATCTCGGAGCTAAGAGGCCCTGTTTTG
R L P G Y M S R L P Q P P E V S Q L G Q I V R L I S E S K R P V L

901 TACGTTGGTGGTGGAAGCTTGAAGCTCGAGTGAAGAACTGGGGAGATTGTGCGAGCTTACTGGGATCCCTGTTGCGAGTACGCTGATGGGGCTTGGCTCTT
Y V G G G S L N S S E E L G R F V E L T G I P V A S T L M G L G S

1001 ATCCTTGTAACGATGAGTTGTCCCTGCAGATGCTTGGCATGCACGGGACTGTGTATGCTAACTACGCTGTGGAGCATAGTGATTGTTGCTGGCGTTTGG
Y P C N D E L S L Q M L G M H G T V Y A N Y A V E H S D L L L A F G

1101 TGTTAGGTTTGTATGACCGTGTACGGGAAAGCTCGAGGCGTTTTCGAGCAGGGCTAAGATTGTGCACATAGACATTGATTCTGCTGAGATTGGGAAGAAT
V R F D D R V T G K L E A F A S R A K I V H I D I D S A E I G K N

1201 AAGACACCTCAGTGTCTGTGTGTGGTGTGTAAAGCTGGCTTTGCAAGGGATGAACAAGGTTCTTGAGAACCGGGCGGAGGAGCTCAAGCTTGATTTTCG
K T P H V S V C G D V K L A L Q G M N K V L E N R A E E L K L D F

1301 GTGTTTGGAGGAGTGAGTTGAGCGAGCAGAAACAGAAGTCCCGTTGAGCTTCAAAACGTTTGGAGAAGCCATTCTCCGCGATACGCGATTACGGTCTCCT
G V W R S E L S E Q K Q K F P L S F K T F G E A I P P Q Y A I Q V L

1401 AGACGAGCTAACCCAGGGAAGGCAATTATCAGNACTGGTGTGGACAGCATCAGATGTGGGCGGCGAGTTTACAAGTACAGGAAGCCGAGGCGAGTGG
D E L T Q G K A I I X T G V G Q H Q M W A A Q F Y K Y R K P R Q W

1501 CTGTCGTCCTCAGGACTCGGAGCTATGGGTTTCGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATGCGATTGTTGTGGACATTGACGGTG
L S S S G L G A M G F G L P A A I G A S V A N P D A I V V D I D G

1601 ATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCACAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTGTTAAACAACCAGCATCTTGGGATGGT
D G S F I M N V Q E L A T I R V E N L P V K I L L L N N Q H L G M V

1701 CATGCAATTGGAAGATCGGTTCTACAAAGCTAACAGAGCTCACACTTATCTCGGGACCCGGCAAGGGAGAACGAGATCTTCCCTAACATGCTGCAGTTT
M Q L E D R F Y K A N R A H T Y L G D P A R E N E I F P N M L Q F

1801 GCAGGAGCTTGCGGGATTCCAGCTGCGAGAGTGACGAAGAAAGAAGAACTCCGAGAAGCTATTACAGACAATGCTGGATACACCTGGACCGTACCTGTTGG
A G A C G I P A A R V T K K E E L R E A I Q T M L D T P G P Y L L

1901 ATGCCATCTGTCCGACCAAGAACATGTGTTACCGATGATCCCAAGTGGTGGCACTTTCAAAGATGTAATAACCGAAGGGGATGGTCGCACTAAGTACTG
D A I C P H Q E H V L P M I P S G G T F K D V I T E G D G R T K Y

2001 AGAGATGAAGCTGGTGATCCATCGTATGGTAAAAGACTTAGTTTCAGTTTTCAGTTTCTTTGTGTGGTAATTTGGGTTTGTGAGTTGTTGTTGTCTT

2101 TGGTTTGTTCCKNAC

Figure 1B

Figure 1C

**T-AHAS3 (SEQ ID NO: 4) nucleotide sequence and
translated amino acid sequence (SEQ ID NO: 104)**

1 TTMACATCTCTCTCATNCACTCTCTCCCTCATCTAACCATGGCGGGCGCAACATCGCCTTCTCCGATCTCCTTAACCGCTAAACCTTCTTCCAAAT
M A A A T S P S P I S L T A K P S S K

101 CCCCTCTACCCATTTCCAGATTCTCCCTTCCCTTCTCCTTAACCCACAGAAACCTCTCCCGTCTCCACCGTCCACTCGCCATCTCCGCCGTTCTCAA
S P L P I S R F S L P F S L T P Q K P S S R L H R P L A I S A V L N

201 CTCACCCGTCAATGTGCGACCTGAAAAAACCGACAAGATCAAGACTTTTCATCTCCCGCTACGCTCCCGACGAGCCCCGCAAGGGTGCTGATATCCTCGTG
S P V N V A P E K T D K I K T F I S R Y A P D E P R K G A D I L V

301 GAAGCCCTCGAGCGTCAAGGCGTCAAGAACCGTCTTCGCTTATCCCGGAGGTGCCTCCATGGAGATCCACCAAGCCTTGACTCGCTCCTCCACCATCCGTA
E A L E R Q G V E T V F A Y P G G A S M E I H Q A L T R S S T I R

401 ACGTCTCCCCCGTCACGAACAAGGAGGAGTCTTCGCGCGCGAGGGTTACGCTCGTTCCTCCGGCAAACCGGAATCTGCATAGCCACTTCGGGTCCTCGG
N V L P R H E Q G G V F A A E G Y A R S S G K P G I C I A T S G P G

501 AGCTACCAACCTCGTCAGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCCTCTCGTCGCCATCACAGGACAGGTCCCTCGCCGGATGATCGGTACTGAC
A T N L V S G L A D A M L D S V P L V A I T G Q V P R R M I G T D

601 GCGTTCCAAGAGACGCCAATCGTTGAGGTAAACGAGGTCTATTACGAAACATAACTATCTGGTGATGGATGTTGATGACATACCTAGGATCGTTCAAGAAG
A F Q E T P I V E V T R S I T K H N Y L V M D V D D I P R I V Q E

701 CATTCTTTCTAGCTACTTCCGGTAGACCCGACCGGTTTTGGTTGATGTTCTTAAGGATATTTCAGCAGCAGCTTGCGATTCTTAAGTGGATCAACCTAT
A F F L A T S G R P G P V L V D V P K D I Q Q Q L A I P N W D Q P M

801 GCGCTTGCTGGTACATGTCTAGGCTGCTCAGCCACCGGAAGTTTCTCAGTTAGGCCAGATCGTTAGGTTGATCTCGGAGTCTAAGAGGCTGTTTTG
R L P G Y M S R L P Q P P E V S Q L G Q I V R L I S E S K R P V L

901 TACGTTGGTGGTGAAGCTTGAACCTCGAGTGAGGAAGTGGGGAGATTGTGCGAGCTTACTGGGATCCCTGTTGCGAGTACGTTGATGGGGCTTGGCTCTT
Y V G G G S L N S S E E L G R F V E L T G I P V A S T L M G L G S

1001 ATCCTTGTAACGATGAGTTGTCCCTGCAGATGCTTGGCATGCACGGGACTGTGTATGCTAACTACGCTGTGGAGCATAGTGATTGTTGCTGGCGTTTGG
Y P C N D E L S L Q M L G M H G T V Y A N Y A V E H S D L L L A F G

1101 TGTTAGGTTTGATGACCGTGTACGCGGAAAGCTCGAGGCGTTTGCAGCAGGGCTAAGATTGTGCACATAGACATTGATTCTGCTGAGATTGGGAAGAAT
V R F D D R V T G K L E A F A S R A K I V H I D I D S A E I G K N

1201 AAGACACCTCAGTGTCTGTGTGGTGTGTAAGCTGGCTTTGCAAGGGATGAACAAGGTTCTTGAGAACCGGGCGGAGGAGCTCAAGCTTGATTTGCG
K T P H V S V C G D V K L A L Q G M N K V L E N R A E E L K L D F

1301 GTGTTTGGAGGAGTGAGTTGAGCGAGCAGAAACAGAAGTTCCCGTTGAGCTTCAAACGTTTGGAGAAGCCATTCTCCGAGTACGCGATTACAGTCTCT
G V W R S E L S E Q K Q K F P L S F K T F G E A I P P Q Y A I Q V L

1401 AGACGAGCTAACCCAAAGGGAAGCAATTATCAGTACTGGTGTGGACAGCATCAGATGTGGCGCGCAGTTTACAAGTACAGGAAGCCGAGGCAGTGG
D E L T Q G K A I I S T G V G Q H Q M W A A Q F Y K Y R K P R Q W

1501 CTGTCGTCCTCAGGACTCGGAGCTATGGGTTTTCGGAATCTCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATGCGATTGTTGTGGACATTGACGGTG
L S S S G L G A M G F G L P A A I G A S V A N P D A I V V D I D G

1601 ATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCACAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGATGGT
D G S F I M N V Q E L A T I R V E N L P V K I L L L N N Q H L G M V

1701 CATGCAATGGGAAGATCGGTTTACAAAGCTAACAGAGCTCACACTTATCTCGGGGACCCGCAAGGGAGAACGAGATCTTCCCTAACATGCTGCAGTTT
M Q W E D R F Y K A N R A H T Y L G D P A R E N E I F P N M L Q F

1801 GCAGGAGCTTTCGGGATTCAGCTGCGAGAGTGACGAAGAAAGAACTCCGAGAAGCTATTACAGACAATGCTGGATACACCTGGACCGTACCTGTTGG
A G A C G I P A A R V T K K E E L R E A I Q T M L D T P G P Y L L

1901 ATGTCTCTGTCCGACCAAGAACATGTGTTACCGATGATCCCAAGTGGTGGCACTTTTCAAGATGTAATAACCGAAGGGGATGGTCCGACTAAGTACTG
D V I C P H Q E H V L P M I P S G G T F E D V I T E G D G R T K Y

2001 AGAGATGAAGCTGGTGTATCCATCATATGGTAAAAGACTTAGTTTCAGTTTACAGTTTCTTTGTGTGGTAATTTGGGTTTGTGAGTTGTGTTCTGCTTT

2101 TGGTTTGTTCCTCCWKAC

Figure 1D

List of oligonucleotides suitable for detection of the PM1 and PM2 mutations. All oligonucleotides are in 5'-3' orientation.

SEQ ID NO.	AHAS1-PM1 forward	SEQ ID NO.	AHAS1-PM1 reverse	SEQ ID NO.	AHAS3-PM2 forward	SEQ ID NO.	AHAS3-PM2 reverse
5	TTATCTCGGGACCGGCA	24	CATCTTTGAAGTGCACCA	47	CTCAGGACTCGGAGCTATGG	66	CTTTGTAGAACCGATCTTCC
6	GACCCGGCAAGGGAGAACGA	25	TCTGTTATTACATCTTTGAA	48	GGAGCTATGGTTTCGGACT	67	GCTCTGTTAGCTTTTGTAGAA
7	GGGAGAACGAGATCTTCCCT	26	ACCATCCCTTCTTGTATTAA	49	GTTCGGACTTCCTGCTCGG	68	ATAAGTGTGAGCTCTGTGTAG
8	GATCTTCCCTAACATGCTGC	27	ACTTAGTCGACCATCCCT	50	TCCTGTGCGATTGGAGGCT	69	GGTCCCCGAGATAAGTGTGA
9	AACATGCTGCAGTTTGCAGG	28	ATCTCTCAGTACTTGTAGTG	51	ATTGGAGCGTCTGTGGCGAA	70	TCCCTTGCCGGTCCCGGAG
10	AGTTTGCAGGAGCTTGCAGG	29	CACGAGCTTCATCTCTCAGT	52	CTGTGGCGAACCCCTGATCGG	71	GATCTGTTCTCCCTTGCCG
11	AGCTTGGGGATTCAGCTG	30	TATGATCGATCACCGACTTC	53	CCCTGATGCGATTGTTGG	72	TGTTAGGGAAGATCTCGTTC
12	ATTCCAGCTGGAGAGTGAC	31	TCCTTTACCATATGATCGAT	54	ATTGTTGTGCACATGACGG	73	AATGCAGCATGTTAGGGAA
13	CGAGAGTGACGAAGAAAGAA	32	TGAACTAAGTCTTTTACCA	55	ACATTGACGGTGATGGAAAGC	74	AGCTCCTGCAAACTGCAGCA
14	GAAGAAAGAACTCCGAG	33	AAC TGGAACACTGAAACTAAG	56	TGATGGAAGCTTCAATAATGA	75	GAATCCCGCAAGCTCCTGCA
15	GAATCCGAGAAGCTATTCA	34	ACACAAAAGAACTGGAAC	57	TTCATAATGAACGTTCAAGA	76	CTCGAGCTGGAATCCCGCA
16	AAGCTATTGACACAAATGCTG	35	CCAAATTTACCACACAAAAGA	58	ACGTTTCAAGAGCTGGCCACA	77	CTTCGTCACTCTCGCAGCTG
17	GACAATGCTGGATACACCAG	36	ACTGACAAACCCAAATTACC	59	GCTGGCCACAATCCGTGTAG	78	GTTCCTTCTTCTTCTCGTCACT
18	GATACACCGAGACCATACCT	37	TAGTACAACTGACAAAC	60	ATCCGTGTAGAGAACTTCC	79	GCTTCTCGGAGTCTTCTTT
19	GACCATACCTGTTGGATGTG	38	CAACCAAAAGTAGTACAAAC	61	AGAACTCTTCTGTGAAGATA	80	TGCTGAAATAGCTTCTCGGA
20	GTTGGATGTATATGTCGCG	39	CGTCTGGGAACCAACCAAAAG	62	TGTGAAGATACTCTTGTAA	81	TATCCAGCATTTGCTGAATA
21	ATATGTCGCGACCAAGAACAA	40	ACAGCGAGTAGCTCTGGGAA	63	CTCTTGTTTAAACAACCAAGCA	82	GGTCCAGGTGTATCCAGCAT
22	ACCAAGAACATGTGTTACCG	41	CAAAACAACACAGCGAGTA	64	ACAACGAGCATCTTTGGGATG	83	CAACAGGTACGGTCCAGGTG
23	TGTGTTACCGATGATCCCAA	42	AAAAAGGAAACAAACAAACA	65	TCTTGGGATGGTTCATGCAAT	84	AGATGACATCCCAACAGGTAC
43	ATGATCCCAAGTGTGGCACT	44	AGTGCCACCACTTGGGATCAT	85	GTCATGCAATGGGAAGATCGG	86	CCGATCTTCCCATTTGCATGAC
45	ATGATCCCAAAATGTGGCACT	46	AGTGCCACCAATTTGGGATCAT	87	GTCATGCAATTTGGAAGATCGG	88	CCGATCTTCCCAATTTGCATGAC

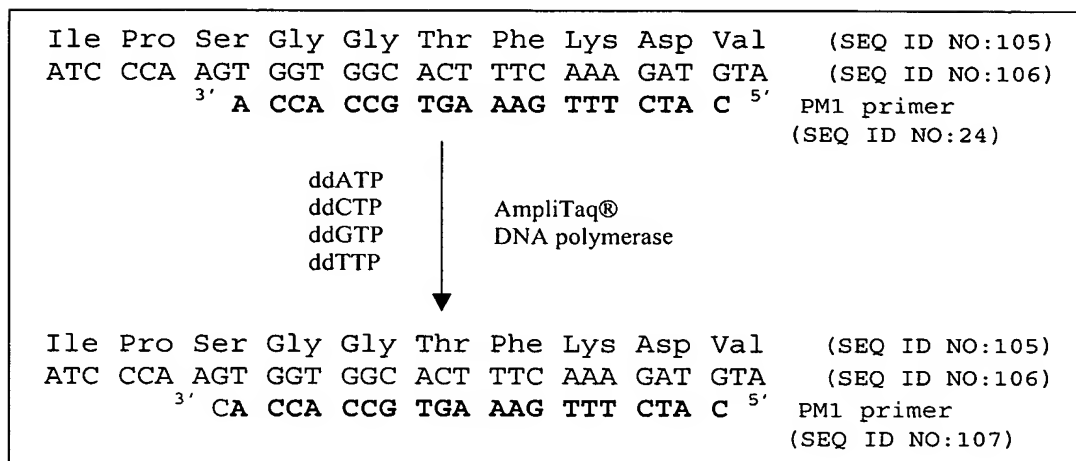
All oligonucleotides noted as being in the forward direction are located on the 5' side of either PM1 or PM2 mutation, in reference to SEQ ID:1 and SEQ ID:2. All oligonucleotides noted as being in the reverse direction are located on the 3' side of either the PM1 or PM2 mutation, in reference to SEQ ID:3 and SEQ ID:4.

Figure 1E

“PM1” Test

AHAS1

‘Topas’



‘PM1’

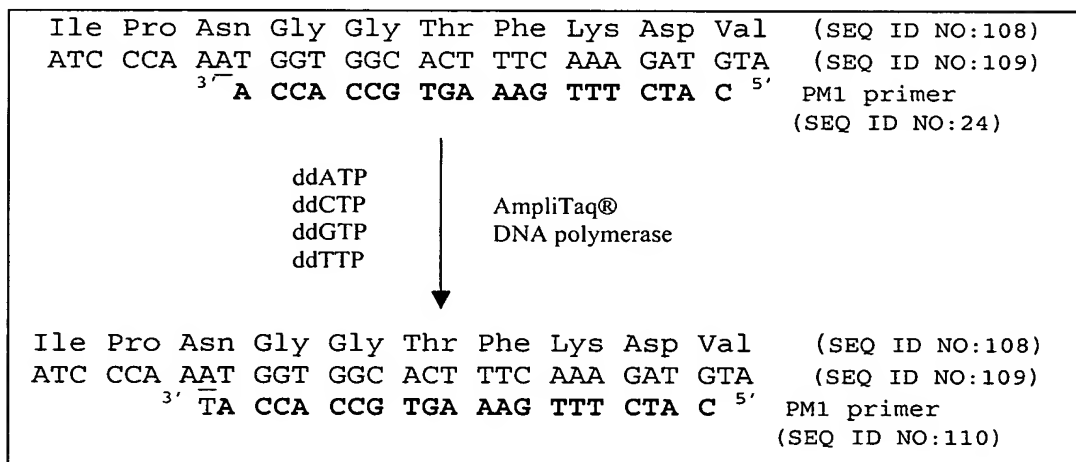
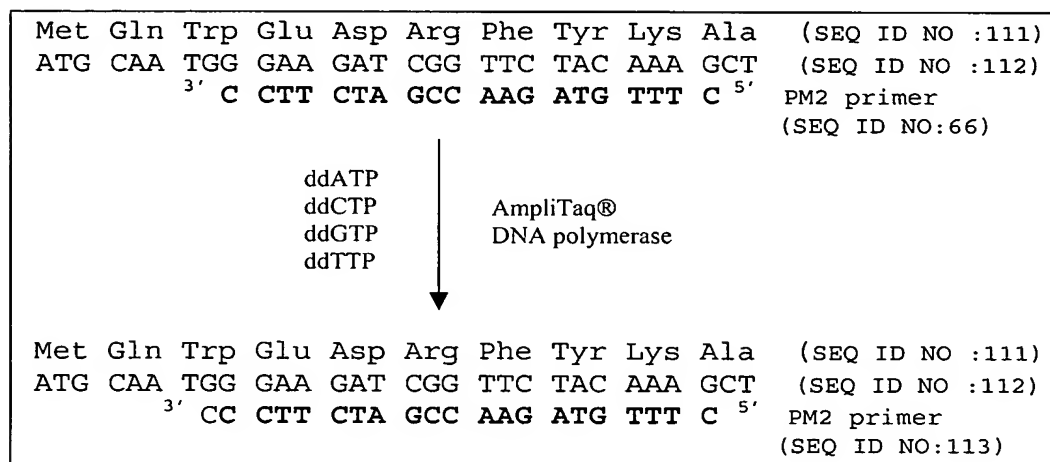


Figure 2

“PM2” Test

AHAS3

‘Topas’



‘PM2’

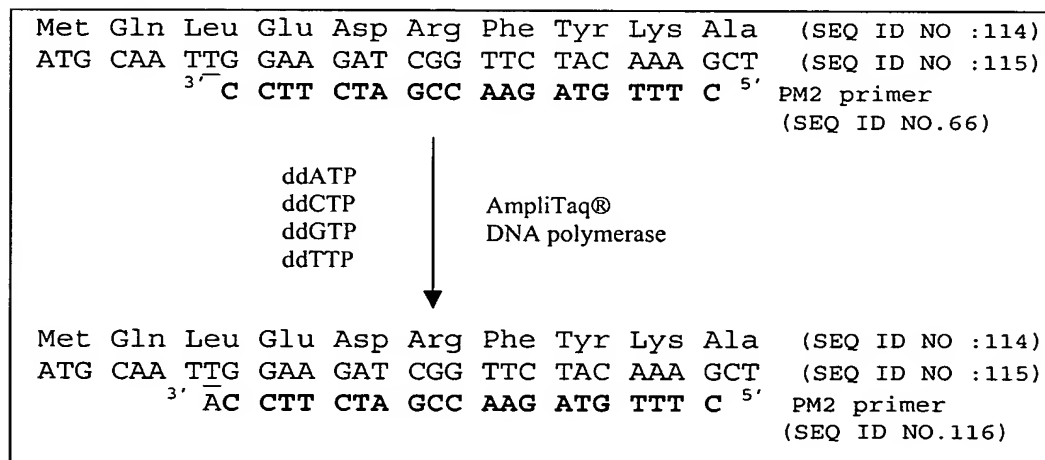


Figure 3

Doubled Haploid Canola Lines		
Plant number	class	GH Rating
1	"PM1/PM2"	0
2	"PM1/PM2"	0
3	"PM1/PM2"	0
4	"PM1/PM2"	0
6	"PM1/PM2"	5
7	"PM1/PM2"	5
37	"PM2"	20
38	"PM2"	20
39	"PM2"	20
40	"PM2"	25
41	"PM2"	25
42	"PM2"	25
68	"PM1"	40
69	"PM1"	40
70	"PM1"	40
71	"PM1"	40
72	"PM1"	40
73	"PM1"	45
103	WT	80
104	WT	80
105	WT	80
106	WT	80
107	WT	85
108	WT	85
-	"PM1"	-
-	"PM2"	-
-	WT	-

Figure 4

Summary of results from “PM1” and “PM2” mutation tests with three replicates using the ABI PRISM® Technology

DNA class	Plant number ²	“PM1” mutation test			“PM2” mutation test		
		Observed ³	Expected ⁴	“PM1” mutation	Observed ³	Expected ⁴	“PM2” mutation
“PM1/PM2” class	1	(C)- <i>T</i>	C- <i>T</i>	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	2	(C)- <i>T</i>	C- <i>T</i>	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	3	(C)- <i>T</i>	C- <i>T</i>	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	4	(C)- <i>T</i>	C- <i>T</i>	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	6	(C)- <i>T</i>	C- <i>T</i>	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	7	(C)- <i>T</i>	C- <i>T</i>	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	37	(C)- <i>T</i>	C	yes	(C)- <i>A</i>	C- <i>A</i>	yes
“PM2” class	38	(C)- <i>T</i>	C	yes	C- <i>A</i>	C- <i>A</i>	yes
	39	(C)- <i>T</i> -(A)	C	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	40	C	C	no	(C)- <i>A</i>	C- <i>A</i>	yes
	41	(C)- <i>T</i>	C	yes	(C)- <i>A</i>	C- <i>A</i>	yes/no
	42	(C)- <i>T</i>	C	yes	(C)- <i>A</i>	C- <i>A</i>	yes
	68	T	C- <i>T</i>	yes	C	C	no
“PM1” class	69	<i>T</i>	C- <i>T</i>	yes	C	C	no
	70	<i>T</i>	C- <i>T</i>	yes	C	C	no
	71	<i>T</i>	C- <i>T</i>	yes	C	C	no
	72	<i>T</i>	C- <i>T</i>	yes	C	C	no
	73	<i>T</i>	C- <i>T</i>	yes	C	C	no
	103	C	C	no	C	C	no
“WT” class	104	C	C	no	C	C	no
	105	C	C	no	C	C	no
	106	C	C	no	C	C	no
	107	C	C	no	C	C	no
	108	C	C	no	C	C	no
	-	(C)- <i>T</i>	C- <i>T</i>	yes	C	C	no
‘PM1’ control ¹	-	C	C	no	C- <i>A</i>	C- <i>A</i>	yes
‘PM2’ control ¹	-	C	C	no	C	C	no
‘Topas’ (WT) control ¹	-	C	C	no	C	C	no

¹‘PM1’ control and ‘PM2’ control are DNA isolated from “PM1” and “PM2” plants used to develop the tests.

²This number refers to the plant number for DH line identified in Figure 4

³In **Bold** and *italics* are the peaks related to the mutations and in brackets are the peaks that are not always present in all the three replicates.

⁴Expected results assuming that the AHAS amplification reaction using AHAS1/AHAS3 amplification primers (SED ID NO:90 and 91) amplified similar amounts of both *AHAS1* and *AHAS3* sequences and that the PM1 extension primers will anneal also to the *AHAS3* sequence and the PM2 extension primers will anneal also to the *AHAS1* sequence.

Figure 5

Summary of results from “PM1” and “PM2” mutation tests using the Pyrosequencing PSQ™96 Technology

DNA sample	“PM1” mutation test		“PM2” mutation test		SEQ ID NO	“PM2” Mutation
	Pyrosequencing results	SEQ ID NO	Pyrosequencing results	“PM1” Mutation		
‘PM1’	CAAA TGGTGG	98	GGGAAAGATC	Yes	99	No
‘PM2’	CAAGTGGTGG	97	TGGAAAGATC	No	100	Yes
‘Topas’ (WT)	CAAGTGGTGG	97	GGGAAAGATC	No	99	No

FIGURE 6